



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/560,494D

Source: 1600

Date Processed by STIC: 6/8/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 4.2 PROGRAM ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
U.S. Patent and Trademark Office, 220 20th Street S.; Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby,
Room 1B03, Arlington, VA 22202

Revised 05/17/04

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/560,494D

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
(OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
(NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- X Use of <220> Sequence(s) 32 missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 0001/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- PatentIn 2.0
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

Best Available Copy



IFW16

RAW SEQUENCE LISTING

DATE: 06/08/2004

PATENT APPLICATION: US/09/560,494D

TIME: 15:06:15

Input Set : A:\102286.413US1.txt

Output Set: N:\CRF4\06082004\I560494D.raw

4 <110> APPLICANT: Jakobsen, Brent Karsten
 5 Gao, George Fu
 6 Gerth, Ulrich Conrad
 7 Sewell, Andrew Kelvin
 9 <120> TITLE OF INVENTION: CD8 AS AN INHIBITOR OF THE CELLULAR IMMUNE SYSTEM
 11 <130> FILE REFERENCE: 102286.413
 13 <140> CURRENT APPLICATION NUMBER: US 09/560,494D
 14 <141> CURRENT FILING DATE: 2000-04-28
 16 <150> PRIOR APPLICATION NUMBER: PCT/GB98/03235
 17 <151> PRIOR FILING DATE: 1998-10-28
 19 <150> PRIOR APPLICATION NUMBER: GB 9722779.7
 20 <151> PRIOR FILING DATE: 1997-10-28
 22 <160> NUMBER OF SEQ ID NOS: 32
 24 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 26 <210> SEQ ID NO: 1
 27 <211> LENGTH: 48
 28 <212> TYPE: DNA
 29 <213> ORGANISM: Artificial Sequence
 31 <220> FEATURE:
 32 <223> OTHER INFORMATION: Synthetic DNA primer
 34 <400> SEQUENCE: 1
 35 gactgagtcg cggccgctgc caccatggcc ttaccagtga ccgccttg 48
 37 <210> SEQ ID NO: 2
 38 <211> LENGTH: 42
 39 <212> TYPE: DNA
 40 <213> ORGANISM: Artificial Sequence
 42 <220> FEATURE:
 43 <223> OTHER INFORMATION: Synthetic DNA primer
 45 <400> SEQUENCE: 2
 46 tattcgactg gatccttata cgtatctcgc cgaaaggctg gg 42
 48 <210> SEQ ID NO: 3
 49 <211> LENGTH: 42
 50 <212> TYPE: DNA
 51 <213> ORGANISM: Artificial Sequence
 53 <220> FEATURE:
 54 <223> OTHER INFORMATION: Synthetic DNA primer
 56 <400> SEQUENCE: 3
 57 ggaattccat atgagccagt tccgggtgtc gccgctggat cg 42
 59 <210> SEQ ID NO: 4
 60 <211> LENGTH: 54
 61 <212> TYPE: DNA
 62 <213> ORGANISM: Artificial Sequence
 64 <220> FEATURE:

Does Not Comply
Corrected Diskette Needed

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Input Set : A:\102286.413US1.txt

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65 <223> OTHER INFORMATION: Synthetic DNA primer
67 <400> SEQUENCE: 4
68 cgcggatccc tatgcgcccc ccgctggccg gctcgccctct gggcgcaggg acag      54
70 <210> SEQ ID NO: 5
71 <211> LENGTH: 60
72 <212> TYPE: DNA
73 <213> ORGANISM: Artificial Sequence
75 <220> FEATURE:
76 <223> OTHER INFORMATION: Synthetic DNA primer
78 <400> SEQUENCE: 5
79 caccgcgaat tcggatccta agcgggtcta caagcttcgg gcttcgctgg caggaagacc 60
82 <210> SEQ ID NO: 6
83 <211> LENGTH: 59
84 <212> TYPE: DNA
85 <213> ORGANISM: Artificial Sequence
87 <220> FEATURE:
88 <223> OTHER INFORMATION: Synthetic DNA primer
90 <400> SEQUENCE: 6
91 caccgcgaat tcggatccta agcgggtcta caagcttctg gcgctcgtgg gggcttcgc 59
93 <210> SEQ ID NO: 7
94 <211> LENGTH: 60
95 <212> TYPE: DNA
96 <213> ORGANISM: Artificial Sequence
98 <220> FEATURE:
99 <223> OTHER INFORMATION: Synthetic DNA primer
101 <400> SEQUENCE: 7
102 caccgcgaat tcggatccta agcgggtcta caagcttcgg gcttcgctgg caggaagacc 60
105 <210> SEQ ID NO: 8
106 <211> LENGTH: 42
107 <212> TYPE: DNA
108 <213> ORGANISM: Artificial Sequence
110 <220> FEATURE:
111 <223> OTHER INFORMATION: Synthetic DNA primer
113 <400> SEQUENCE: 8
114 gtggcaagct tggatcctat ggcgtcgtgg tgggcttcgc tg      42
116 <210> SEQ ID NO: 9
117 <211> LENGTH: 42
118 <212> TYPE: DNA
119 <213> ORGANISM: Artificial Sequence
121 <220> FEATURE:
122 <223> OTHER INFORMATION: Synthetic DNA primer
124 <400> SEQUENCE: 9
125 ggaattccat atgagtcaat ttcgtgtatc accgctggat cg      42
127 <210> SEQ ID NO: 10
128 <211> LENGTH: 35
129 <212> TYPE: DNA
130 <213> ORGANISM: Artificial Sequence
132 <220> FEATURE:
133 <223> OTHER INFORMATION: Synthetic DNA primer

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Input Set : A:\102286.413US1.txt

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135 <400> SEQUENCE: 10
136 acatacccat gggctctcac tccatgaggt atttc 35
138 <210> SEQ ID NO: 11
139 <211> LENGTH: 43
140 <212> TYPE: DNA
141 <213> ORGANISM: Artificial Sequence
143 <220> FEATURE:
144 <223> OTHER INFORMATION: Synthetic DNA primer
146 <400> SEQUENCE: 11
147 acatacaagc ttacggctcc catcttaagg tgaggggctt ggg 43
149 <210> SEQ ID NO: 12
150 <211> LENGTH: 9
151 <212> TYPE: PRT
152 <213> ORGANISM: Artificial Sequence
154 <220> FEATURE:
155 <223> OTHER INFORMATION: HLA-A2 Pol-restricted CTL line specific peptide
157 <400> SEQUENCE: 12
158 Ile Leu Lys Glu Pro Val His Gly Val
159 1 5
-----162-<210>-SEQ ID NO: 13-----
163 <211> LENGTH: 9
164 <212> TYPE: PRT
165 <213> ORGANISM: Artificial Sequence
167 <220> FEATURE:
168 <223> OTHER INFORMATION: HLA-A2 Pol-restricted CTL line specific peptide
170 <400> SEQUENCE: 13
171 Ser Leu Tyr Asn Thr Val Ala Thr Leu
172 1 5
175 <210> SEQ ID NO: 14
176 <211> LENGTH: 9
177 <212> TYPE: PRT
178 <213> ORGANISM: Artificial Sequence
180 <220> FEATURE:
181 <223> OTHER INFORMATION: HLA-A2 Pol-restricted CTL line specific peptide
183 <400> SEQUENCE: 14
184 Val Ile Tyr Gln Tyr Met Asp Asp Leu
185 1 5
188 <210> SEQ ID NO: 15
189 <211> LENGTH: 42
190 <212> TYPE: DNA
191 <213> ORGANISM: Artificial Sequence
193 <220> FEATURE:
194 <223> OTHER INFORMATION: Synthetic DNA primer
196 <400> SEQUENCE: 15
197 ctgtccaacc cgacgtcggg cagctcgtgg ctcttcaccg cg 42
199 <210> SEQ ID NO: 16
200 <211> LENGTH: 42
201 <212> TYPE: DNA
202 <213> ORGANISM: Artificial Sequence

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204 <220> FEATURE:
205 <223> OTHER INFORMATION: Synthetic DNA primer
207 <400> SEQUENCE: 16
208 cggctggaag agccacgagc tgcccgcacgt cgggttgac ag          42
210 <210> SEQ ID NO: 17
211 <211> LENGTH: 99
212 <212> TYPE: DNA
213 <213> ORGANISM: Artificial Sequence
215 <220> FEATURE:
216 <223> OTHER INFORMATION: Synthetic DNA primer
218 <400> SEQUENCE: 17
219 gggggaagct taatgccatt cgattttctg agcttcaaaa atatcggttca gaccaccacc 60
220 ggatcctggc gtcgtggtgg gcttcgctgg caggaagac          99
222 <210> SEQ ID NO: 18
223 <211> LENGTH: 18
224 <212> TYPE: PRT
225 <213> ORGANISM: Artificial Sequence
227 <220> FEATURE:
228 <223> OTHER INFORMATION: CD8 alpha polypeptide
230 <400> SEQUENCE: 18
231 Gly Ser Gly Gly Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu
232 1          5          10          15
233 Trp His
237 <210> SEQ ID NO: 19
238 <211> LENGTH: 63
239 <212> TYPE: DNA
240 <213> ORGANISM: Artificial Sequence
242 <220> FEATURE:
243 <223> OTHER INFORMATION: Synthetic DNA primer
245 <400> SEQUENCE: 19
246 gaggaggagc atatgaaacc acaagcacct gaactacgaa tctttccaaa gaaaatggac 60
247 gcc          63
249 <210> SEQ ID NO: 20
250 <211> LENGTH: 36
251 <212> TYPE: DNA
252 <213> ORGANISM: Artificial Sequence
254 <220> FEATURE:
255 <223> OTHER INFORMATION: synthetic DNA primer
257 <400> SEQUENCE: 20
258 ggggagggaa gcttacttgg tagtagtaga gtccac          36
260 <210> SEQ ID NO: 21
261 <211> LENGTH: 9
262 <212> TYPE: PRT
263 <213> ORGANISM: Artificial Sequence
265 <220> FEATURE:
266 <223> OTHER INFORMATION: HLA-A2-flu
268 <400> SEQUENCE: 21
269 Gly Ile Leu Gly Phe Val Phe Thr Leu
270 1          5

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Input Set : A:\102286.413US1.txt

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273 <210> SEQ ID NO: 22
274 <211> LENGTH: 9
275 <212> TYPE: PRT
276 <213> ORGANISM: Artificial Sequence
278 <220> FEATURE:
279 <223> OTHER INFORMATION: peptide epitope
281 <400> SEQUENCE: 22
282 Lys Ala Val Tyr Asn Phe Ala Thr Cys
283 1 5
286 <210> SEQ ID NO: 23
287 <211> LENGTH: 366
288 <212> TYPE: DNA
289 <213> ORGANISM: Artificial Sequence
291 <220> FEATURE:
292 <223> OTHER INFORMATION: synthetic DNA construct encoding part of the
293 extracellular domain of human CD8 alpha
W--> 295 <221> NAME/KEY: CDS
296 <222> LOCATION: (1)...(366)
W--> 298 <400> 23
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299 atg agt caa ttt cgt gta tca ccg ctg gat cgg acc tgg aac ctg ggc 48
300 Met Ser Gln Phe Arg Val Ser Pro Leu Asp Arg Thr Trp Asn Leu Gly
301 1 5 10 15
303 gag aca gtg gag ctg aag tgc cag gtg ctg ctg tcc aac ccg acg tgc 96
304 Glu Thr Val Glu Leu Lys Cys Gln Val Leu Leu Ser Asn Pro Thr Ser
305 20 25 30
307 ggc tgc tgc tgg ctc ttc cag ccg cgc ggc gcc gcc gcc agt ccc acc 144
308 Gly Cys Ser Trp Leu Phe Gln Pro Arg Gly Ala Ala Ala Ser Pro Thr
309 35 40 45
311 ttc ctc cta tac ctc tcc caa aac aag ccc aag gcg gcc gag ggg ctg 192
312 Phe Leu Leu Tyr Leu Ser Gln Asn Lys Pro Lys Ala Ala Glu Gly Leu
313 50 55 60
315 gac acc cag cgg ttc tgc ggc aag agg ttg ggg gac acc ttc gtc ctc 240
316 Asp Thr Gln Arg Phe Ser Gly Lys Arg Leu Gly Asp Thr Phe Val Leu
317 65 70 75 80
319 acc ctg agc gac ttc cgc cga gag aac gag ggc tac tat ttc tgc tgc 288
320 Thr Leu Ser Asp Phe Arg Arg Glu Asn Glu Gly Tyr Tyr Phe Cys Ser
321 85 90 95
323 gcc ctg agc aac tcc atc atg tac ttc agc cac ttc gtg ccg gtc ttc 336
324 Ala Leu Ser Asn Ser Ile Met Tyr Phe Ser His Phe Val Pro Val Phe
325 100 105 110
327 ctg cca gcg aag ccc acc acg acg cca tag 366
328 Leu Pro Ala Lys Pro Thr Thr Thr Pro *
329 115 120
332 <210> SEQ ID NO: 24
333 <211> LENGTH: 121
334 <212> TYPE: PRT
335 <213> ORGANISM: Artificial Sequence
337 <220> FEATURE:
338 <223> OTHER INFORMATION: an amino acid construct encoding part of the

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<210> SEQ ID NO 32

<211> LENGTH: 247

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: :

See item 11 on error
summary report.

<400> SEQUENCE: 32

Met	Ala	Ser	Pro	Leu	Thr	Arg	Phe	Leu	Ser	Leu	Asn	Leu	Leu	Leu	Leu
1				5				10				15			
Gly	Glu	Ser	Ile	Ile	Leu	Gly	Ser	Gly	Glu	Ala	Lys	Pro	Gln	Ala	Pro
			20					25				30			
Glu	Leu	Arg	Ile	Phe	Pro	Lys	Lys	Met	Asp	Ala	Glu	Leu	Gly	Gln	Lys
			35				40					45			

RAW SEQUENCE LISTING ERROR SUMMARY
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Use of <220> Feature(NEW RULES):

Sequence(s) are missing the <220> Feature and associated headings.

Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32) (Sec.1.823 of new Rules)

Seq#:23,25,31,32

VERIFICATION SUMMARY

DATE: 06/08/2004

PATENT APPLICATION: US/09/560,494D

TIME: 15:06:16

Input Set : A:\102286.413US1.txt

Output Set: N:\CRF4\06082004\I560494D.raw

L:295 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:298 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:23
L:369 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:372 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:25
L:478 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:29
L:585 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:588 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:31
L:659 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:32, <213>
ORGANISM:Artificial Sequence
L:659 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:32, <213>
ORGANISM:Artificial Sequence
L:659 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:32,Line#:659
